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MAY 25 2001

TECH CENTER 1600/2900

SEQUENCE LISTING



<110> Otsuka Pharmaceutical Co., Ltd.

<120> HUMAN P51 GENES AND GENE PRODUCTS THEREOF

<130> Q61014

<140> 09/670,568

<141> 2000-09-27

<150> JP 10-100467

<151> 1998-03-27

<160> 23

<170> PatentIn version 3.0

<210> 1

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<212> PRT

<213> Homo sapiens

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<223> transactivation domain

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<223> DNA binding domain

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<223> oligomerization domain

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Ser Asp Pro Met Trp Pro Gln Tyr Thr Asn Leu Gly Leu Leu Asn Ser  
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 Thr Asp His Ala Gln Asn Ser Val Thr Ala Pro Ser Pro Tyr Ala Gln  
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 Pro Ser Ser Thr Phe Asp Ala Leu Ser Pro Ser Pro Ala Ile Pro Ser  
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 Asn Thr Asp Tyr Pro Gly Pro His Ser Phe Asp Val Ser Phe Gln Gln  
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 Ser Ser Thr Ala Lys Ser Ala Thr Trp Thr Tyr Ser Thr Glu Leu Lys  
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 Met Thr Pro Pro Pro Gln Gly Ala Val Ile Arg Ala Met Pro Val Tyr  
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 Glu Leu Ser Arg Glu Phe Asn Glu Gly Gln Ile Ala Pro Pro Ser His  
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 Gly Thr Glu Phe Thr Thr Val Leu Tyr Asn Phe Met Cys Asn Ser Ser  
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Ile Asp Leu Asn Phe Val Asp Glu Pro Ser Glu Asp Gly Ala Thr Asn  
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Lys Ile Glu Ile Ser Met Asp Cys Ile Arg Met Gln Asp Ser Asp Leu  
50 55 60

Ser Asp Pro Met Trp Pro Gln Tyr Thr Asn Leu Gly Leu Leu Asn Ser  
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Met Asp Gln Gln Ile Gln Asn Gly Ser Ser Ser Thr Ser Pro Tyr Asn  
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Thr Asp His Ala Gln Asn Ser Val Thr Ala Pro Ser Pro Tyr Ala Gln  
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 Lys Arg Arg Ser Pro Asp Asp Glu Leu Leu Tyr Leu Pro Val Arg Gly  
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 Arg Glu Thr Tyr Glu Met Leu Leu Lys Ile Lys Glu Ser Leu Glu Leu  
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 Leu Ala Ser Leu Lys Ile Pro Glu Gln Phe Arg His Ala Ile Trp Lys  
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 Gly Ile Leu Asp His Arg Gln Leu His Glu Phe Ser Ser Pro Ser His  
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Thr Tyr Ser Thr Glu Leu Lys Lys Leu Tyr Cys Gln Ile Ala Lys Thr

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Cys Pro Ile Gln Ile Lys Val Met Thr Pro Pro Pro Gln Gly Ala Val

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atc cgc gcc atg cct gtc tac aaa aaa gct gag cac gtc acg gag gtg Ile Arg Ala Met Pro Val Tyr Lys Lys Ala Glu His Val Thr Glu Val	190	195	200	747
gtg aag cgg tgc ccc aac cat gag ctg agc cgt gaa ttc aac gag gga Val Lys Arg Cys Pro Asn His Glu Leu Ser Arg Glu Phe Asn Glu Gly	205	210	215	795
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Glu Thr Tyr Arg Gln Gln Gln Gln Gln Gln His Gln His Leu Leu Gln	
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 620 625 630

cag cgc atc aaa gag gag ggg gag tgagcctcac catgtgagct cttcctatcc 2097  
 Gln Arg Ile Lys Glu Glu Gly Glu  
 635 640

ctctcctaac tgccagcccc ctaaaagcac tcctgcttaa tcttcaaagc cttctcccta 2157

gctcctcccc ttcctcttgt ctgatttctt aggggaagga gaagtaagag gctacctctt 2217

acctaacatc tgacctggca tctaattctg attctggctt taagccttca aaa 2270

<210> 6  
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Met Ser Gln Ser Thr Gln Thr Asn Glu Phe Leu Ser Pro Glu Val Phe  
 1 5 10 15

Gln His Ile Trp Asp Phe Leu Glu Gln Pro Ile Cys Ser Val Gln Pro  
 20 25 30

Ile Asp Leu Asn Phe Val Asp Glu Pro Ser Glu Asp Gly Ala Thr Asn  
 35 40 45

Lys Ile Glu Ile Ser Met Asp Cys Ile Arg Met Gln Asp Ser Asp Leu  
 50 55 60

Ser Asp Pro Met Trp Pro Gln Tyr Thr Asn Leu Gly Leu Leu Asn Ser  
 65 70 75 80

Met Asp Gln Gln Ile Gln Asn Gly Ser Ser Ser Thr Ser Pro Tyr Asn  
 85 90 95

Thr Asp His Ala Gln Asn Ser Val Thr Ala Pro Ser Pro Tyr Ala Gln  
 100 105 110

Pro Ser Ser Thr Phe Asp Ala Leu Ser Pro Ser Pro Ala Ile Pro Ser  
 115 120 125

Asn Thr Asp Tyr Pro Gly Pro His Ser Phe Asp Val Ser Phe Gln Gln  
 130 135 140

Ser Ser Thr Ala Lys Ser Ala Thr Trp Thr Tyr Ser Thr Glu Leu Lys  
 145 150 155 160

Lys Leu Tyr Cys Gln Ile Ala Lys Thr Cys Pro Ile Gln Ile Lys Val  
 165 170 175

Met Thr Pro Pro Pro Gln Gly Ala Val Ile Arg Ala Met Pro Val Tyr  
 180 185 190  
 Lys Lys Ala Glu His Val Thr Glu Val Val Lys Arg Cys Pro Asn His  
 195 200 205  
 Glu Leu Ser Arg Glu Phe Asn Glu Gly Gln Ile Ala Pro Pro Ser His  
 210 215 220  
 Leu Ile Arg Val Glu Gly Asn Ser His Ala Gln Tyr Val Glu Asp Pro  
 225 230 235 240  
 Ile Thr Gly Arg Gln Ser Val Leu Val Pro Tyr Glu Pro Pro Gln Val  
 245 250 255  
 Gly Thr Glu Phe Thr Thr Val Leu Tyr Asn Phe Met Cys Asn Ser Ser  
 260 265 270  
 Cys Val Gly Gly Met Asn Arg Arg Pro Ile Leu Ile Ile Val Thr Leu  
 275 280 285  
 Glu Thr Arg Asp Gly Gln Val Leu Gly Arg Arg Cys Phe Glu Ala Arg  
 290 295 300  
 Ile Cys Ala Cys Pro Gly Arg Asp Arg Lys Ala Asp Glu Asp Ser Ile  
 305 310 315 320  
 Arg Lys Gln Gln Val Ser Asp Ser Thr Lys Asn Gly Asp Gly Thr Lys  
 325 330 335  
 Arg Pro Phe Arg Gln Asn Thr His Gly Ile Gln Met Thr Ser Ile Lys  
 340 345 350  
 Lys Arg Arg Ser Pro Asp Asp Glu Leu Leu Tyr Leu Pro Val Arg Gly  
 355 360 365  
 Arg Glu Thr Tyr Glu Met Leu Leu Lys Ile Lys Glu Ser Leu Glu Leu  
 370 375 380  
 Met Gln Tyr Leu Pro Gln His Thr Ile Glu Thr Tyr Arg Gln Gln Gln  
 385 390 395 400  
 Gln Gln Gln His Gln His Leu Leu Gln Lys Gln Thr Ser Ile Gln Ser  
 405 410 415  
 Pro Ser Ser Tyr Gly Asn Ser Ser Pro Pro Leu Asn Lys Met Asn Ser  
 420 425 430  
 Met Asn Lys Leu Pro Ser Val Ser Gln Leu Ile Asn Pro Gln Gln Arg  
 435 440 445  
 Asn Ala Leu Thr Pro Thr Thr Ile Pro Asp Gly Met Gly Ala Asn Ile  
 450 455 460  
 Pro Met Met Gly Thr His Met Pro Met Ala Gly Asp Met Asn Gly Leu

465                      470                      475                      480  
 Ser Pro Thr Gln Ala Leu Pro Pro Pro Leu Ser Met Pro Ser Thr Ser  
                                  485                      490                      495  
 His Cys Thr Pro Pro Pro Pro Tyr Pro Thr Asp Cys Ser Ile Val Ser  
                                  500                      505                      510  
 Phe Leu Ala Arg Leu Gly Cys Ser Ser Cys Leu Asp Tyr Phe Thr Thr  
                                  515                      520                      525  
 Gln Gly Leu Thr Thr Ile Tyr Gln Ile Glu His Tyr Ser Met Asp Asp  
                                  530                      535                      540  
 Leu Ala Ser Leu Lys Ile Pro Glu Gln Phe Arg His Ala Ile Trp Lys  
 545                      550                      555                      560  
 Gly Ile Leu Asp His Arg Gln Leu His Glu Phe Ser Ser Pro Ser His  
                                  565                      570                      575  
 Leu Leu Arg Thr Pro Ser Ser Ala Ser Thr Val Ser Val Gly Ser Ser  
                                  580                      585                      590  
 Glu Thr Arg Gly Glu Arg Val Ile Asp Ala Val Arg Phe Thr Leu Arg  
                                  595                      600                      605  
 Gln Thr Ile Ser Phe Pro Pro Arg Asp Glu Trp Asn Asp Phe Asn Phe  
                                  610                      615                      620  
 Asp Met Asp Ala Arg Arg Asn Lys Gln Gln Arg Ile Lys Glu Glu Gly  
 625                      630                      635                      640  
 Glu

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27

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<220>  
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29

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<220>  
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<220>  
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D7  
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<220>  
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<220>  
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<210> 13  
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<212> DNA  
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cgcgtggtct gtgttatagg 20

<210> 14  
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D7  
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Wk  
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ccacctggac gtattccact 20

<210> 17  
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18

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<223> Description of Artificial Sequence: p51-F4 sense primer

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19

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<211> 20

<212> DNA

<213> Artificial Sequence

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<223> Description of Artificial Sequence: p51-R4 antisense primer

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20

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<223> Description of Artificial Sequence: p51-F5 sense primer

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<223> Description of Artificial Sequence: p51-R5 antisense primer

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<223> Description of Artificial Sequence: p51-F6 sense primer

<400> 22

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D7  
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<211> 20

<212> DNA

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W  
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<223> Description of Artificial Sequence: p51-R6 antisense primer

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ctagtggctt tgtgcctttg

20